SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Hadlaczky, Gyula
Szalay, Aladar

(ii) TITLE OF THE INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES

(iii) NUMBER OF SEQUENCES: 34

(iv) CORRESPONDENCE ADDRESS:
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(C) CITY: La Jolla
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 92037

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE: 28-NOV-2000

(vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/835,682
(B) FILING DATE: 10-APR-1997
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/695,191
(B) FILING DATE: 07-AUG-1996
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/682,080
(B) FILING DATE: 15-JUL-1996
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/629,822
(B) FILING DATE: 10-APR-1996
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Seidman, Stephanie L
(B) REGISTRATION NUMBER: 33,779
(C) REFERENCE/DOCKET NUMBER: 24601-402G

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 858-450-8403
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(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1293 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
GAATTCATCA TTTTTCANGT CCTCAAGTGG ATGTTTCTCA TTTNCCATGA TTTTAAGTTT     60
TCTCGCCATA TTCCTGGTCC TACAGTGTGC ATTTCTCCAT TTTNCACGTT TTNCAGTGAT    120
TTCGTCATTT TCAAGTCCTC AAGTGGATGT TTCTCATTTN CCATGAATTT CAGTTTTCTN    180
GCCATATTCC ACGTCCTACA GNGGACATTT CTAAATTTNC CACCTTTTTC AGTTTTCCTC    240
GCCATATTTC ACGTCCTAAA ATGTGTATTT CTCGTTTNCC GTGATTTTCA GTTTTCTCGC    300
CAGATTCCAG GTCCTATAAT GTGCATTTCT CATTTNNCAC GTTTTTCAGT GATTTCGTCA    360
TTTTTTCAAG TCGGCAAGTG GATGTTTCTC ATTTNCCATG ATTTNCAGTT TTCTTGNAAT    420
ATTCCATGTC CTACAATGAT CATTTTTAAT TTTCCACCTT TTCATTTTTC CACGCCATAT    480
TTCATGTCCT AAAGTGTATA TTTCTCCTTT TCCGCGATTT TCAGTTTTCT CGCCATATTC    540
CAGGTCCTAC AGTGTGCATT CCTCATTTTT CACCTTTTTC ACTGATTTCG TCATTTTTCA    600
AGTCGTCAAC TGGATCTTTC TAATTTTCCA TGATTTTCAG TTATCTTGTC ATATTCCATG    660
TCCTACAGTG GACATTTCTA AATTTTCCAA CTTTTTCAAT TTTTCTCGAC ATATTTGACG    720
TGCTAAAGTG TGTATTTCTT ATTTTCCGTG ATTTTCAGTT TTCTCGCCAT ATTCCAGGTC    780
CTAATAGTGT GCATTTCTCA TTTTTCACGT TTTTCAGTGA TTTCGTCATT TTTTCCAGTT    840
GTCAAGGGGA TGTTTCTCAT TTTCCATGAG TGTCAGTTTT CTTGCTATAT TCCATGTCCT    900
ACAGTGACAT TTCTAAATAT TATACCTTTT TCAGTTTTTC TCACCATATT TCACGTCCTA    960
AAGTATATAT TTCTCATTTT CCCTGATTTT CAGTTTCCTT GCCATATTCC AGGTCCTACA   1020
GTGTGCATTT CTCATTTTTC ACGTTTTTCA GTAATTTCTT CATTTTTTAA GCCCTCAAAT   1080
GGATGTTTCT CATTTTCCAT GATTTTCAGT TTTCTTGCCA TATACCATGT CCTACAGTGG   1140
ACATTTCTAA ATTATCCACC TTTTTCAGTT TTTCATCGGC ACATTTCACG TCCTAAAGTG   1200
TGTATTTCTA ATTTTCAGTG ATTTTCAGTT TTCTCGCCAT ATTCCAGGAC CTACAGTGTG   1260
CATTTCTCAT TTTTCACGTT TTTCAGTGAA TTC                                1293
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1044 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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AGGCCTATGG TGAAAAAGGA AATATCTTCC CCTGAAAACT AGACAGAAGG ATTCTCAGAA     60
TCTTATTTGT GATGTGCGCC CCTCAACTAA CAGTGTTGAA GCTTTCTTTT GATAGAGCAG    120
TTTTGAAACA CTCTTTTTGT AAAATCTGCA AGAGGATATT TGGATAGCTT TGAGGATTTC    180
CGTTGGAAAC GGGATTGTCT TCATATAAAC CCTAGACAGA AGCATTCTCA GAAGCTTCAT    240
TGGGATGTTT CAGTTGAAGT CACAGTGTTG AACAGTCCCC TTTCATAGAG CAGGTTTGAA    300
ACACTCTTTT TTGTAGTATC TGGAAGTGGA CATTTGGAGC GATCTCAGGA CTGCGGTGAA    360
AAAGGAAATA TCTTCCAATA AAAGCTAGAT AGAGGCAATG TCAGAAACCT TTTTCATGAT    420
GTATCTACTC AGCTAACAGA GTTGAACCTT CCTTTGAGAG AGCAGTTTTG AAACACTCTT    480
TTTGTGGAAT CTGCAAGTGG ATATTTGTCT AGCTTTGAGG ATTTCGTTGG GAAACGGGAT    540
TACATATAAA AAGCAGACAG CAGCATTCCC AGAAACTTCT TTGTGATGTT TGCATTCAAG    600
TCACAGAGTT GAACATTCCC TTTCATAGAG CAGGTTTGAA ACACACTTTT TGATGTATCT    660
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GGATGTGGAC ATTTGCAGCG CTTTCAGGCC TAAGGTGAAA AGGAAATATC TTCCCCTGAA 720
AACTAGACAG AAGCATTCTC AGAAACTTAT TTGTGATGTG CGCCCTCAAC TAACAGTGTT 780
GAAGCTTTCT TTTGATAGAG GCAGTTTTGA AACACTCTTT TGTGGAATCT GCAAGTGGAT 840
ATTTGTCTAG CTTTGAGGAT TTCTTTGGAA ACGGGATTAC ATATAAAAAG CAGACAGCAG 900
CATTCCCAGA ATCTTGTTTG TGATGTTTGC ATTCAAGTCA CAGAGTTGAA CATTCCCTTT 960
CAGAGAGCAG GTTTGAACAC TCTTTTTATA GTATCTGGAT GTGGACATTT GGAGCGCTTT 1020
CAGGGGGGAT CCTCTAGAAT TCCT 1044

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2492 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTGCAGCTGG GGGTCTCCAA TCAGGCAGGG GCCCCTTACT ACTCAGATGG GGTGGCCGAG 60
TAGGGGAAGG GGGTGCAGGC TGCATGAGTG GACACAGCTG TAGGACTACC TGGGGGCTGT 120
GGATCTATGG GGGTGGGGAG AAGCCCAGTG ACAGTGCCTA GAAGAGACAA GGTGGCCTGA 180
GAGGGTCTGA GGAACATAGA GCTGGCCATG TTGGGGCCAG GTCTCAAGCA GGAAGTGAGG 240
AATGGGACAG GCTTGAGGAT ACTCTACTCA GTAGCCAGGA TAGCAAGGAG GGCTTGGGGT 300
TGCTATCCTG GGGTTCAACC CCCCAGGTTG AAGGCCCTGG GGGAGATGGT CCCAGGACAT 360
ATTACAATGG ACACAGGAGG TTGGGACACC TGGAGTCACC AAACAAAACC ATGCCAAGAG 420
AGACCATGAG TAGGGGTGTC CAGTCCAGCC CTCTGACTGA GCTGCATTGT TCAAATCCAA 480
AGGGCCCCTG CTGCCACCTA GTGGCTGATG GCATCCACAT GACCCTGGGC CACACGCGTT 540
TAGGGTCTCT GTGAAGACCA AGATCCTTGT TACATTGAAC GACTCCTAAA TGAGCAGAGA 600
TTTCCACCTA TTCGAAACAA TCACATAAAA TCCATCCTGG AAAAAGCCTG GGGGATGGCA 660
CTAAGGCTAG GGATAGGGTG GGATGAAGAT TATAGTTACA GTAAGGGGTT TAGGGTTAGG 720
GATCAACGTT GGTTAGGAGT TAGGGATACA GTAGGGTACC GGTAGGGTTA GGGGTTAGGG 780
TTAGGGGTTA GGGTTAGGGT TAGGGTTAGG GTTAGGGTTA GGGGTTAGGG GTTAGGGTTA 840
GGGTTAGGTT TTGGGGTGGC GTATTTTGGT CTTATACGCT GTGTTCCACT GGCAATGAAA 900
AGAGTTCTTG TTTTTCCTTC AGCAATTTGT CATTTTTAAA AGAGTTTAGC AATTCTAACA 960
GATATAGACC AGCTGTGCTA TCTCATTGTG GTTTTCAATT GTAACCACAT TGTGGTTTCA 1020
ATGTGTTTAC TTGCCATCTG TAGATCTTCT TTGCGTGAGG TGTCTGTTCA GATGTGTGTG 1080
CATTTCTTGN NTTTNGGCTG TTTAACTTAT TGTTTAGTTT TAATAATTTT TTATATATTT 1140
GAAGACAAAT CTTTCTCAGA TGTGTATTTG CAAATATTTC TTCAATATGA GGCTTGCTTT 1200
TGTCTCTAAC AAGGTCTCTT CAGAGATAAC TTAAATATAA GAAATCCACA CTGTCACTTC 1260
TTTTGTGTAT ATCTACCTTT TGTGTCATTT GTTAAAATTC ATTACCAAAC CCAAAGGCAG 1320
ATAGCTTTTC TTCTATTGTT TCTTCTAGAA ATTTGTATAG TTTTGCATTT TTAGTGTAAG 1380
GATGATTTTG AGTGATTATT TGTGTAAGTT GTAAAGTTTT CGTCTATATC CATATCATTT 1440
CTTATGGTTT CCAATTAATC GTTCCCTCAC TATTTTTGGG AAAGACACAG GATAGTGGGC 1500
TTTGTTAGAG TAGATAGGTA GCTAGACATG AACAGGAGGG GGCCTCCTGG AAAAGGGAAA 1560
GTCTGGGAAG GCTCACCTGG AGGACCACCA AAAATTCACA TATTAGTAGC ATCTCTAGTG 1620
CTGGAGTGGA TGGGCACTTG TCAATTGTGG GTAGGAGGGA AAAGAGGTCC TATGCAGAAA 1680
GAAACTCCCT AGAACTCCTC TGAAGATGCC CCAATCATTC ACTCTGCAAT AAAAATGTCA 1740
GAATATTGCT AGCTACATGC TGATAAGGNN AAAGGGGACA TTCTTAAGTG AAACCTGGCA 1800
CCATAAGTAC AGATTAGGGC AGAGAAGGAC ATTCAAAAGA GGCAGGCGCA GTAGGTACAA 1860
ACGTGATCGC TGTCAGTGTG CCTGGGATGG CGGGAAGGAG GCTGGTGCCA GAGTGGATTC 1920
GTATTGATCA CCACACATAT ACCTCAACCA ACAGTGAGGA GGTCCCACAA GCCTAAGTGG 1980
GGCAAGTTGG GGAGCTAAGG CAGTAGCAGG AAAACCAGAC AAAGAAAACA GGTGGAGACT 2040
TGAGACAGAG GCAGGAATGT GAAGAAATCC AAAATAAAAT TCCCTGCACA GGACTCTTAG 2100
GCTGTTTAAT GCATCGCTCA GTCCCACTCC TCCCTATTTT TCTACAATAA ACTCTTTACA 2160
CTGTGTTTCT TTTCAATGAA GTTATCTGCC ATCTTTGTAT TGCCTCTTGG TGAAAATGTT 2220
TCTTCCAAGT TAAACAAGAA CTGGGACATC AGCTCTCCCC AGTAATAGCT CCGTTTCAGT 2280

TTGAATTTAC AGAACTGATG GGCTTAATAA CTGGCGCTCT GACTTTAGTG GTGCAGGAGG 2340
CCGTCACACC GGGACCAAGA GTGCCCTGCC TAGTCCCCAT CTGCCCGCAG GTGGCGGCTG 2400
CCTCGACACT GACAGCAATA GGGTCCGGCA GTGTCCCCAG CTGCCAGCAG GGGGCGTACG 2460
ACGACTACAC TGTGAGCAAG AGGGCCCTGC AG 2492

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGGGAATTCA TTGGGATGTT TCAGTTGA 28

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGAAAGTCCC CCCTAGGAGA TCTTAAGGA 29

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCGCTTAATA CTCTGATGAG TCCGTGAGGA CGAAACGCTC TCGCACC

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGATTTAAAT TAATTAAGCC CGGGC 25

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TAAATTTAAT TAATTCGGGC CCGTCGA 27

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(D) OTHER INFORMATION IL-2 signal sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG TAC AGG ATG CAA CTC CTG TCT TGC ATT GCA CTA AGT CTT GCA CTT 48
Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu

GTC ACA AAC AGT GCA CCT ACT 69
Val Thr Asn Ser Ala Pro Thr

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 945 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 1...942
(D) OTHER INFORMATION: Renilla Reinformis Luciferase

(x) PUBLICATION INFORMATION:

PATENT NO.: 5,418,155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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AGC TTA AAG ATG ACT TCG AAA GTT TAT GAT CCA GAA CAA AGG AAA CGG      48
Ser Leu Lys Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg
 1               5                  10                  15

ATG ATA ACT GGT CCG CAG TGG TGG GCC AGA TGT AAA CAA ATG AAT GTT      96
Met Ile Thr Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val
            20                  25                  30

CTT GAT TCA TTT ATT AAT TAT TAT GAT TCA GAA AAA CAT GCA GAA AAT     144
Leu Asp Ser Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn
        35                  40                  45

GCT GTT ATT TTT TTA CAT GGT AAC GCG GCC TCT TCT TAT TTA TGG CGA     192
Ala Val Ile Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg
    50                  55                  60

CAT GTT GTG CCA CAT ATT GAG CCA GTA GCG CGG TGT ATT ATA CCA GAT     240
His Val Val Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp
65                  70                  75                  80

CTT ATT GGT ATG GGC AAA TCA GGC AAA TCT GGT AAT GGT TCT TAT AGG     288
Leu Ile Gly Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg
                85                  90                  95

TTA CTT GAT CAT TAC AAA TAT CTT ACT GCA TGG TTG AAC TTC TTA ATT     336
Leu Leu Asp His Tyr Lys Tyr Leu Thr Ala Trp Leu Asn Phe Leu Ile
            100                 105                 110

TAC CAA AGA AGA TCA TTT TTT GTC GGC CAT GAT TGG GGT GCT TGT TTG     384
Tyr Gln Arg Arg Ser Phe Phe Val Gly His Asp Trp Gly Ala Cys Leu
        115                 120                 125

GCA TTT CAT TAT AGC TAT GAG CAT CAA GAT AAG ATC AAA GCA ATA GTT     432
Ala Phe His Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val
    130                 135                 140

CAC GCT GAA AGT GTA GTA GAT GTG ATT GAA TCA TGG GAT GAA TGG CCT     480
His Ala Glu Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro
145                 150                 155                 160

GAT ATT GAA GAA GAT ATT GCG TTG ATC AAA TCT GAA GAA GGA GAA AAA     528
Asp Ile Glu Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys
                165                 170                 175

ATG GTT TTG GAG AAT AAC TTC TTC GTG GAA ACC ATG TTG CCA TCA AAA     576
Met Val Leu Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys
            180                 185                 190

ATC ATG AGA AAG TTA GAA CCA GAA GAA TTT GCA GCA TAT CTT GAA CCA     624
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Ile Met Arg Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro
        195                 200                 205

TTC AAA GAG AAA GGT GAA GTT CGT CGT CCA ACA TTA TCA TGG CCT CGT      672
Phe Lys Glu Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg
    210                 215                 220

GAA ATC CCG TTA GTA AAA GGT GGT AAA CCT GAC GTT GTA CAA ATT GTT      720
Glu Ile Pro Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val
225                 230                 235                 240

AGG AAT TAT AAT GCT TAT CTA CGT GCA AGT GAT GAT TTA CCA AAA ATG      768
Arg Asn Tyr Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met
                245                 250                 255

TTT ATT GAA TCG GAT CCA GGA TTC TTT TCC AAT GCT ATT GTT GAA GGC      816
Phe Ile Glu Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly
            260                 265                 270

GCC AAG AAG TTT CCT AAT ACT GAA TTT GTC AAA GTA AAA GGT CTT CAT      864
Ala Lys Lys Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His
        275                 280                 285

TTT TCG CAA GAA GAT GCA CCT GAT GAA ATG GGA AAA TAT ATC AAA TCG      912
Phe Ser Gln Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser
    290                 295                 300

TTC GTT GAG CGA GTT CTC AAA AAT GAA CAA TAA                         945
Phe Val Glu Arg Val Leu Lys Asn Glu Gln
305                 310
```

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```
TTTGAATTC A TGTACAGGAT GCAACTCCTG                                   30
```

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTTGAATTCA GTAGGTGCAC TGTTTGTCAC 30

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1434 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCTCCACGCA CGTTGTGATA TGTAGATGAT AATCATTATC AGAGCAGCGT TGGGGGATAA 60
TGTCGACATT TCCACTCCCA ATGACGGTGA TGTATAATGC TCAAGTATTC TCCTGCTTTT 120
TTACCACTAA CTAGGAACTG GGTTTGGCCT TAATTCAGAC AGCCTTGGCT CTGTCTGGAC 180
AGGTCCAGAC GACTGACACC ATTAACACTT TGTCAGCCTC AGTGACTACA GTCATAGATG 240
AACAGGCCTC AGCTAATGTC AAGATACAGA GAGGTCTCAT GCTGGTTAAT CAACTCATAG 300
ATCTTGTCCA GATACAACTA GATGTATTAT GACAAATAAC TCAGCAGGGA TGTGAACAAA 360
AGTTTCCGGG ATTGTGTGTT ATTTCCATTC AGTATGTTAA ATTTACTAGG ACAGCTAATT 420
TGTCAAAAAG TCTTTTTCAG TATATGTTAC AGAATTGGAT GGCTGAATTT GAACAGATCC 480
TTCGGGAATT GAGACTTCAG GTCAACTCCA CGCGCTTGGA CCTGTCGCTG ACCAAAGGAT 540
TACCCAATTG GATCTCCTCA GCATTTTCTT TCTTTAAAAA ATGGGTGGGA TTAATATTAT 600
TTGGAGATAC ACTTTGCTGT GGATTAGTGT TGCTTCTTTG ATTGGTCTGT AAGCTTAAGG 660
CCCAAACTAG GAGAGACAAG GTGGTTATTG CCCAGGCGCT TGCAGGACTA GAACATGGAG 720
CTTCCCCTGA TATATGGTTA TCTATGCTTA GGCAATAGGT CGCTGGCCAC TCAGCTCTTA 780
TATCCCACGA GGCTAGTCTC ATTGTACGGG ATAGAGTGAG TGTGCTTCAG CAGCCCGAGA 840
GAGTTGCAAG GCTAAGCACT GCAATGGAAA GGCTCTGCGG CATATATGTG CCTATTCTAG 900
GGGGACATGT CATCTTTCAT GAAGGTTCAG TGTCCTAGTT CCCTTCCCCC AGGCAAAACG 960
ACACGGGAGC AGGTCAGGGT TGCTCTGGGT AAAAGCCTGT GAGCCTGGGA GCTAATCCTG 1020
TACATGGCTC CTTTACCTAC ACACTGGGGA TTTGACCTCT ATCTCCACTC TCATTAATAT 1080
GGGTGGCCTA TTTGCTCTTA TTAAAAGGAA AGGGGGAGAT GTTGGGAGCC GCGCCCACAT 1140
TCGCCGTTAC AAGATGGCGC TGACAGCTGT GTTCTAAGTG GTAAACAAAT AATCTGCGCA 1200
TGTGCCGAGG GTGGTTCTTC ACTCCATGTG CTCTGCCTTC CCCGTGACGT CAACTCGGCC 1260
GATGGGCTGC AGCCAATCAG GGAGTGACAC GTCCTAGGCG AAGGAGAATT CTCCTTAATA 1320
GGGACGGGGT TTCGTTCTCT CTCTCTCTCT TGCTTCTCTC TCTTGCTTTT TCGCTCTCTT 1380
GCTTCCCGTA AAGTGATAAT GATTATCATC TACATATCAC AACGTGCGTG GAGG 1434

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCTCCACGCA CGTTGTGATA TGTAGATGAT AATCATTATC AGAGCAGCGT TGGGGGATAA 60
TGTCGACATT TCCACTCCCA ATGACGGTGA TGTATAATGC TCAAGTATTC TCCTGCTTTT 120
TTACCACTAA CTAGGAACTG GGTTTGGCCT TAATTCAGAC AGCCTTGGCT CTGTCTGGAC 180
AGGTCCAGAT ACAACTAGAT GTATTATGAC AAATAACTCA GCAGGGATGT GAACAAAAGT 240

TTCCGGGATT GCGTGTTATT TCCATCCAGT ATGTTAAATT TACTAGGGCA GCTAATTTGT 300
CAAAAAGTCT TTTCCAGTAT ATGTTACAGA ATTGGATGGC TGAATTTGAA CAGATCCTTC 360
GGGAATTGAG ACTTCAGGTC AACTCCACGC GCTTGGACCT GTCCCTGACC AAAGGATTAC 420
CCAATTGGAT CTCCTCAGCA TTTTCTTTCT TTAAAAAATG GGTGGGATTA ATATTATTTG 480
GAGATACACT TTGCTGTGGA TTAGTGTTGC TTCTTTGATT GGTCTGTAAG CTTAAGGCCC 540
AAACTAGGAG AGACAAGGTG GTTATTGCCC AGGCGCTTGC AGGACTAGAA CATGGAGCTT 600
CCCCTGATAT ATCTATGCTT AGGCAATAGG TCGCTGGCCA CTCAGCTCTT ATATCCCATG 660
AGGCTAGTCT CATTGCACGG GATAGAGTGA GTGTGCTTCA GCAGCCCGAG AGAGTTGCAC 720
GGCTAAGCAC TGCAATGGAA AGGCTCTGCG GCATATATGA GCCTATTCTA GGGAGACATG 780
TCATCTTTCA AGAAGGTTGA GTGTCCAAGT GTCCTTCCTC CAGGCAAAAC GACACGGGAG 840
CAGGTCAGGG TTGCTCTGGG TAAAAGCCTG TGAGCCTAAG AGCTAATCCT GTACATGGCT 900
CCTTTACCTA CACACTGGGG ATTTGACCTC TATCTCCACT CTCATTAATA TGGGTGGCCT 960
ATTTGCTCTT ATTAAAAGGA AAGGGGGAGA TGTTGGGAGC CGCGCCCACA TTCGCCGTTA 1020
CAAGATGGCG CTGACAGCTG TGTTCTAAGT GGTAAACAAA TAATCTGCGC ATGCGCCGAG 1080
GGTGGTTCTT CACTCCATGT GCTCTGCCTT CCCCGTGACG TCAACTCGGC CGATGGGCTG 1140
CAGTCAATCA GGGAGTGACA CGTCCTAGGC GAAGGAAAAT TCTCCTTAAT AGGGACGGGG 1200
TTTCGTTTTC TCTCTCTCTT GCTTCGCTCT CTCTTGCTTC TTGCTCTCTT TTCCTGAAGA 1260
TGTAAGAATA AAGCTTTGCC GCAGAAGATT CTGGTCTGTG GTGTTCTTCC TGGCCGGTCG 1320
TGAGAACGCG TCTAATAACA ATTGGTGCCG AAACCCGGGT GATAATGATT ATCATCTACA 1380
TATCACAACG TGCGTGGAGG 1400

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1369 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCTCCACGCA CGTTGTGATA TGTAGATGAT AATCATTATC ACTTTACGGG TCCTTTCACT 60
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ACACATTACT CAAGGTGGGC TCATCTGAGC TGCAGATTCA GCTTAATATG AATCTTGCCA 180
ATTGTGTGAA ATCATAAATC TTCAAAGTGA CACTCATTGC CAGACACAGG TGCCCACCTT 240
TGGCATAATA AACAAACACA AATTATCTAT TATATAAAGG GTGTTAGAAG ATGCTTTAGA 300
ATACAAATAA ATCATGGTAG ATAACAGTAA GTTGAGAGCT TAAATTTAAT AAAGTGATAT 360
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AATTTATTTT CTTTCTTAAT CCTTTATAAT GTTTTCTGCT ATTGTCAATT GCACATCCAT 480
ATGTTCAATT CTTCACTGTA ATGAAGAAAT GTAGTAAATA TACTTTCCGA ACAAGTTGTA 540
TCAAATATGT TACACTTGAT TCCGTGTGTT ACTTATCATT TTATTATTAT ATTGATTGCA 600
TTCCTTCGTT ACTTGATATT ATTACAAGGT ACATATTTAT TCTCTCAGAT CTTCATTATA 660
CTCTAACCAT TTTATAACAT ACTTTATTTA TTCATTTCTT ATGTGTGCTG TGAGGCACAA 720
ATGCCAGAGA GAACTTGAGC AGATAAGAGG ACAAATTGCA AGAGTCAGTT ACCTCCTGCT 780
GTTCCTTGGA AACTCAGGAT CAAATTCAGG TTGTCAGGCT TGGCAGCATG CACTTTTTAC 840
CAGTGCCTCC ATCTTGCTAG CCCTGAACAT CAAGCTTTGC AGACAGACAG GCTACACTAA 900
GTGAACTGGT CATTCACAGC ATGCATGGTG ATTTATTGTT ACTTTCTATT CCATGCCTTT 960
ACTATTTCTA CTAGGTGCTA GCTAGTACTG TATTTCGAGA TAGAAGTTAC TGAAAGAAAA 1020
TTACATTGTT TTCTATAGAT CCTTGATACT CTTTCAGCAG ATATAGAGTT TTAATCAGGT 1080
CCTAGACCCT TTCTTCACTC TTATTAAATA CTAAGTACAA ATTAAGTTTA TCCAAAACAG 1140
TACGGATGTT GATTTTGTGC AGTTCTACTA TGATAATAGT CTAGCTTCAT AAATCTGACA 1200
CACTTATTGG GAATGTTTTT GTTAATAAAA GATTCAGGTG TTACTCTAGG TCAAGAGAAT 1260
ATTAAACATC AGTCCCAAAT TACAAACTTC AATAAAAGAT TTGACTCTCC AGTGGTGGCA 1320
ATATAAAGTG ATAATGATTA TCATCTACAT ATCACAACGT GCGTGGAGG 1369

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22118 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

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CAGACAGACA GACAGACGTT ACAAACAAAC ACGTTGAGCC GTGTGCCAAC ACACACACAA 240
ACACCACTCT GGCCATAATT ATTGAGGACG TTGATTTATT ATTCTGTGTT TGTGAGTCTG 300
TCTGTCTGTC TGTCTGTCTG TCTGTCTGTC TATCAAACCA AAAGAAACCA AACAATTATG 360
CCTGCCTGCC TGCCTGCCTG CCTACACAGA GAAATGATTT CTTCAATCAA TCTAAAACGA 420
CCTCCTAAGT TTGCCTTTTT TCTCTTTCTT TATCTTTTTC TTTTTTCTTT TCTTCTTCCT 480
TCCTTCCTTC CTTCCTTCCT TCCTTCCTTT CTTTCTTTCT TTCTTTCTTT CTTACTTTCT 540
TTCTTTCCTT CTTACATTTA TTCTTTTCAT ACATAGTTTC TTAGTGTAAG CATCCCTGAC 600
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(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42999 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

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TGTAATAAGT CACCCCAAAG ATCACCGTAT CTGACAAAAT AACTACCACA GGGTTATGAC 32640
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CTGCAACCGC CACCTCCCTG GGTTCAAGCG ATTCTCCTGC CTCAGCCTCC CGAGTAGCTG 32820
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ACTATGAAGT CAGTCCAGAG AAACGCAATA AATGTCAACG GTGAGGATGG TGTTGAGGCA 33060
GAAGTAGGAC CACACTTTTT CCTATCTTAT TCAGTTGATA ACAATATGAC CTAGGTAGTA 33120
ATTTCCTATG TGCCTACTTA TACACGAGTA CAAAAGAGTA AAACAGAGAG ACTGCTAAAT 33180
TAAAGGGTAC GTGAAGTTCT TCATAGTAAC TCCGTAAACT GGAACACTGT CAAAAAGCAG 33240
CAGCTAGTGA ATTGTTTCCA TGTATTTTTC TATTATCCAA TAAGTGAACT ATGCTATTCC 33300
TTTCCAGTCT CCCAAGCACT TCTTGTCCCC ATCACCACTT CGGTGCTCGA AGAAAAAGTA 33360
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CAAGCTAATG CTTTGTCCAG TTCTTCAGTG AAGACAACTC ACGCCCTAAT GCGCTATAGG 33780
CATAAGCATC ATTTGGATCC ACTTCGAGAG TTCTCTGGAA GAATTGAATC GCAATATCGT 33840
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GGGATTTTAG GTGGAAACTT CATTTTTAAT TTTCTCCTAA TTCTCCTCGG TTGTGGAGCT 34440
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CAGAGGAAAG GATTTCAACG AAGGCTCTTT TGGTCACATT CTGATCCTTT GGTAAGCCGA 35220
TCTGTCTTGC AATATACATG TCCCGACGAT GGAAGGGGAA AGCGAGCTGA ATCACCAAAC 35280
TCAGGAACGA TAATATCATC GTGGCTTTTC TGCTTATGAA ACACTCCACC CGATAAGATT 35340
TGATCCCCTT CTGCAAGCTT GCTGAGATCA ACACAACATT TCGCAAGCAG GCATTTGCAT 35400
TGCGGGGTAG TACAACTGTG TCCTTTCAAG AGTCTATATG TTTTATAGGC CTTTCCTGAG 35460
CGGTAAGAAC AGGTCGCCAG TAAGAACAAG GCTTCTTCTG AGTGTACTTC TGCATAAAGG 35520
CGTTCTGCGG GGGAAACCGC ATCTCGGTAG GCATAGTGGT TTAGTGCTTG CCATATAGCA 35580
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GCACCAGCCG CCGTTACCGG GGGATGGGGG AGTCCGAGAC AGAATGACTT CTTTATCCTG 35760
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CGGATGCCCC GAGTGACTGT GGCTCGCACC TCTCCGGAAA CATTGGAAAT CTCTCCTCTA 36120
CGCGCGGCCA CCTGAAACCA CAGGAGCTCG GGACACACGT GCTTTCGGGA GAGAATGCTG 36180
AGAGTCTCTC GCCGACTCTC TCTTGACTTG AGTTCTTCGT GGGTGCGTGG TTAAGACGTA 36240
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CTCTGAAAAC GGAGGCCTCA CAGAGGAAGG GAGCACCAGG CCGCCTGCGC ACAGCCTGGG 38040
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CTAGGAAATC GCCACTTTGA CGACCGGGTC TGATTGACCT TTGATCAGGC AAAAACGAAC 38160
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ATACAATAGG ATACGATACA ATACAATACA ATACAATACA ATACAATACA ATACAATACA 38340
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GATGCCGAGG TGGACGCATC ACCTGAAGTC GGGAGTTGGA GACAAGCCCG ACCAACATGG 38460
AGAAATCCCG TCTCAATTGA AAATACAAAA CTAGCCGGGC GCGGTGGCAC ATGCCTATAA 38520

TCCCAGCTGC TAGGAAGGCT GAGGCAGGAG AATCGCTTGA ACCTGGGAAG CGGAGGTTGC 38580
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AGGAATTATG CGTGATTTCT TTTTTTAACT TCATTTTATG TTATTATCAT GATTGATGTT 39240
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CCCTGGCTGG GCCCGATTGT TCTTCTCCTT GGTCAGGGGT TTCCTTGTCT TTCTTCGTGT 39360
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TGGCCGGCCT TCGGTCCCTC GTGTGTCCCG GTCGTAGGAG GGGCCGGCCG AAAATGCTTC 42720
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TCCGTGTGTG GCTGCGATGG TGGCGTTTTT GGGGACAGGT GTCCGTGTCC GTGTCGCGCG 42900
TCGCCTGGGC CGGCGGCGTG GTCGGTGACG CGACCTCCCG GCCCCGGGGG AGGTATATCT 42960
TTCGCTCCGA GTCGGCAATT TTGGGCCGCC GGGTTATAT 42999

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTCCCGCGCG GCCCCCGTGT TCGCCGTTCC CGTGGCGCGG ACAATGCGGT TGTGCGTCCA 60
CGTGTGCGTG TCCGTGCAGT GCCGTTGTGG AGTGCCTCGC TCTCCTCCTC CTCCCCGGCA 120
GCGTTCCCAC GGTTGGGGAC CACCGGTGAC CTCGCCCTCT TCGGGCCTGG ATCCG 175

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 755 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGTCTGGTGG GAATTGTTGA CCTCGCTCTC GGGTGCGGCC TTTGGGGAAC GGCGGGGTCG 60
GTCGTGCCCG GCGCCGGACG TGTGTCGGGG CCCACTTCCC GCTCGAGGGT GGCGGTGGCG 120
GCGGCGTTGG TAGTCTCCCG TGTTGCGTCT TCCCGGGCTC TTGGGGGGGG TGCCGTCGTT 180
TTCGGGGCCG GCGTTGCTTG GCTTACGCAG GCTTGGTTTG GGACTGCCTC AGGAGTCGTG 240
GGCGGTGTGA TTCCCGCCGG TTTTGCCTCG CGTCTGCCTG CTTTGCCTCG GGTTTGCTTG 300
GTTCGTGTCT CGGGAGCGGT GGTTTTTTTT TTTTTCGGGT CCCGGGGAGA GGGGTTTTTC 360
CGGGGGACGT TCCCGTCGCC CCCTGCCGCC GGTGGGTTTT CGTTTCGGGC TGTGTTCGTT 420
TCCCCTTCCC CGTTTCGCCG TCGGTTCTCC CCGGTCGGTC GGCCCTCTCC CCGGTCGGTC 480
GCCCGGCCGT GCTGCCGGAC CCCCCCTTCT GGGGGGGATG CCCGGGCACG CACGCGTCCG 540
GGCGGCCACT GTGGTCCGGG AGCTGCTCGG CAGGCGGGTG AGCCAGTTGG AGGGGCGTCA 600
TGCCCCCGCG GGCTCCCGTG GCCGACGCGG CGTGTTCTTT GGGGGGGCCT GTGCGTGCGG 660
GAAGGCTGCG CACGTTGTCG GTCCTTGCGA GGGAAAGAGG CTTTTTTTTT TTAGGGGGTC 720
GTCCTTCGTC GTCCCGTCGG CGGTGGATCC GGCCT 755

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 463 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

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GGCCGAGGTG CGTCTGCGGG TTGGGGCTCG TCCGGCCCCG TCGTCCTCCG GGAAGGCGTT     60
TAGCGGGTAC CGTCGCCGCG CCGAGGTGGG CGCACGTCGG TGAGATAACC CCGAGCGTGT    120
TTCTGGTTGT TGGCGGCGGG GGCTCCGGTC GATGTCTTCC CCTCCCCCTC TCCCCGAGGC    180
CAGGTCAGCC TCCGCCTGTG GGCTTCGTCG GCCGTCTCCC CCCCCCTCAC GTCCCTCGCG    240
AGCGAGCCCG TCCGTTCGAC CTTCCTTCCG CCTTCCCCCC ATCTTTCCGC GCTCCGTTGG    300
CCCCGGGGTT TTCACGGCGC CCCCCACGCT CCTCCGCCTC TCCGCCCGTG GTTTGGACGC    360
CTGGTTCCGG TCTCCCCGCC AAACCCCGGT TGGGTTGGTC TCCGGCCCCG GCTTGCTCTT    420
CGGGTCTCCC AACCCCCGGC CGGAAGGGTT CGGGGGTTCC GGG                       463
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(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 378 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

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GGATTCTTCA GGATTGAAAC CCAAACCGGT TCAGTTTCCT TTCCGGCTCC GGCCGGGGGG     60
GGCGGCCCCG GGCGGTTTGG TGAGTTAGAT AACCTCGGGC CGATCGCACG CCCCCCGTGG    120
CGGCGACGAC CCATTCGAAC GTCTGCCCTA TCAACTTTCG ATGGTAGTCG ATGTGCCTAC    180
CATGGTGACC ACGGGTGACG GGGAATCAGG GTTCGATTCC GGAGAGGGAG CCTGAGAAAC    240
GGCTACCACA TCCAAGGAAG GCAGCAGGCG CGCAAATTAC CCACTCCCGA CCCGGGGAGG    300
TAGTGACGAA AAATAACAAT ACAGGACTCT TTCGAGGCCC TGTAATTGGA ATGAGTCCAC    360
TTTAAATCCT TTAAGCAG                                                  378
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(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 378 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

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GATCCATTGG AGGGCAAGTC TGGTGCCAGC AGCCGCGGTA ATTCCAGCTC CAATAGCGTA     60
TATTAAAGTT GCTGCAGTTA AAAAGCTCGT AGTTGGATCT TGGGAGCGGG CGGGCGGTCC    120
GCCGCGAGGC GAGTCACCGC CCGTCCCCGC CCCTTGCCTC TCGGCGCCCC CTCGATGCTC    180
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TTAGCTGAGT TGTCCCGCGG GGCCCGAAGC GTTTACTTTG AAAAAATTAG AGTTGTTTCA 240
AAGCAGGCCC GAGCCGCCTG GATACCGCCA GCTAGGAAAT AATGGAATAG GACCGCGGTT 300
CCTATTTTGT TTGGTTTTCG GAACTGAGCC CATGATTAAG GGAAACGGCC GGGGGCATTC 360
CCTTATTGCG CCCCCCTA 378

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 719 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGATCTTTCC CGCTCCCCGT TCCTCCCGGC CCCTCCACCC GCGCGTCTCC CCCCTTCTTT 60
TCCCCTCTCC GGAGGGGGGG GAGGTGGGGG CGCGTGGGCG GGGTCGGGGG TGGGGTCGGC 120
GGGGGACCGC CCCCGGCCGG CAAAAGGCCG CCGCCGGGCG CACTTCAACC GTAGCGGTGC 180
GCCGCGACCG GCTACGAGAC GGCTGGGAAG GCCCGACGGG GAATGTGGCT CGGGGGGGGC 240
GGCGCGTCTC AGGGCGCGCC GAACCACCTC ACCCCGAGTG TTACAGCCCT CCGGCCGCGC 300
TTTCGCGGAA TCCCGGGGCC GAGGGGAAGC CCGATACCCG TCGCCGCGCT TTTCCCCTCC 360
CCCCGTCCGC CTCCCGGGCG GGCGTGGGGG TGGGGGCCGG GCCGCCCCTC CCACGCCCGT 420
GGTTTCTCTC TCTCCCGGTC TCGGCCGGTT TGGGGGGGGG AGCCCGGTTG GGGGCGGGGC 480
GGACTGTCCT CAGTGCGCCC CGGGCGTCGT CGCGCCGTCG GGCCCGGGGG GTTCTCTCGG 540
TCACGCCGCC CCCGACGAAG CCGAGCGCAC GGGGTCGGCG GCGATGTCGG CTACCCACCC 600
GACCCGTCTT GAAACACGGA CCAAGGAGTC TAACGCGTGC GCGAGTCAGG GGCTCGCACG 660
AAAGCCGCCG TGGCGCAATG AAGGTGAAGG GCCCCGTCCG GGGGCCCGAG GTGGGATCC 719

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 685 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CGAGGCCTCT CCAGTCCGCC GAGGGCGCAC CACCGGCCCG TCTCGCCCGC CGCGTCGGGG 60
AGGTGGAGCA CGAGCGTACG CGTTAGGACC CGAAAGATGG TGAACTATGC CTGGGCAGGG 120
CGAAGCCAGA GGAAACTCTG GTGGAGGTCC GTAGCGGTCC TGACGTGCAA ATCGGTCGTC 180
CGACCTGGGT ATAGGGGCGA AAGACTAATC GAACCATCTA GTAGCTGGTT CCCTCCGAAG 240
TTTCCCTCAG GATAGCTGGC GCTCTCGCAA CCTTCGGAAG CAGTTTTATC CGGGTAAAGG 300
CGGAATGGAT TAGGAGGTCT TGGGGCCGGA AACGATCTCA AACTATTTCT CAAACTTTAA 360
ATGGGTAAGG AAGCCCGGCT CGCTGGCGTG GAGCCGGGCG TGGAATGCGA GTGCCTAGTG 420
GGCCACTTTT GGTAAGCAGA ACTGGCGCTG CGGGATGAAC CGAACGCCGG GTTAAGGCGC 480
CCGATGCCGA CGCTCATCAG ACCCCAGAAA AGGTGTTGGT TGATATAGAC AGCAGGACGG 540
TGGCCATGGA AGTCGGAATC CGCTAAGGAG TGTGTAACAA CTCACCTGCC GAATCAACTA 600
GCCCTGAAAA TGGATGGCGC TGGAGCGTCG GGCCCATACC CGGCCGTCGC CGGCAGTCGG 660
AACGGGACGG GACGGGAGCG GCCGC 685

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GAGGAATTCC CCTATCCCTA ATCCAGATTG GTG 33

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AAACTGCAGG CCGAGCCACC TCTCTTCTGT GTTTG 35

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AGGAATTCAC AGAAGAGAGG TGGCTCGGCC TGC 33

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGCCTGCAGG AAGTCATACC TGGGGAGGTG GCCC 34

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AAACTGCAGG TTAATTAACC CTAACCCTAA CCCTAACCCT AACCCTAACC CTAACCCTAA 60
CCCTAACCCT AACCCGGGAT 80

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTGGGCCCTA GGCTTAAGG 19

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GCCAGGGTTT TCCCAGTCAC GACGT 25

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GCTGCAAGGC GATTAAGTTG GGTAAC 26

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TATGTTGTGT GGAATTGTGA GCGGAT 26

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGGTTTAAAC AGATCTCTGC A 21